

RESULT 1
 US-08-323-474-2
 ; Sequence 2, Application US/08323474
 ; Patent No. 5447860
 ; GENERAL INFORMATION:
 ; APPLICANT: Ziegler, Steven F.
 ; TITLE OF INVENTION: NOVEL TYROSINE KINASE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/323,474
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/905,600
 ; FILING DATE: 26-JUN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seese, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2609
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-323-474-2

Query Match 100.0%; Score 1708; DB 1; Length 1124;
 Best Local Similarity 100.0%; Pred. No. 3e-155;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALNRKVKNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYA 60
 ||||||||||||||||||
 Db 802 ALNRKVKNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYA 861
 ||||||||||||||||||
 Qy 61 SKDDHRDFAGEVLCKLGHHPNIIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLE 120
 ||||||||||||||||||
 Db 862 SKDDHRDFAGEVLCKLGHHPNIIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLE 921
 ||||||||||||||||||
 Qy 121 TDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIA 180
 ||||||||||||||||||
 Db 922 TDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIA 981
 ||||||||||||||||||
 Qy 181 DFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCG 240
 ||||||||||||||||||
 Db 982 DFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCG 1041
 ||||||||||||||||||
 Qy 241 MTCAELYEKLPGQYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKT 300
 ||||||||||||||||||
 Db 1042 MTCAELYEKLPGQYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKT 1101
 ||||||||||||||||||
 Qy 301 YVNTTLYEKFTYAGIDCSAEEAA 323
 ||||||||||||||||||
 Db 1102 YVNTTLYEKFTYAGIDCSAEEAA 1124

Sequence Match Listing

RESULT 1

TIE2_HUMAN

ID TIE2_HUMAN STANDARD; PRT: 1124 AA.
AC Q02763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (P140
DE TEK) (Tunica interna endothelial cell kinase) (CD202b antigen).
GN TEK OR TIE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93173509; PubMed=8382358;
RA Ziegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R.;
RT "Molecular cloning and characterization of a novel receptor protein
RT tyrosine kinase from human placenta.";
RL Oncogene 8:663-670(1993).
RN [2]
RP VARIANT VMCM1 TRP-849.
RX MEDLINE=97134665; PubMed=8980225;
RA Vikkula M., Boon L.M., Cawray K.L. III, Calvert J.T., Diamonti A.J.,
RA Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C.,
RA Mulliken J.B., Olse B.R.;
RT "Vascular dysmorphogenesis caused by an activating mutation in the
RT receptor tyrosine kinase TIE2.";
RL Cell 87:1181-1190(1996).
RN [3]
RP VARIANTS VMCM1 TRP-849 AND SER-897.
RX MEDLINE=99299243; PubMed=10369874;
RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
RA Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Pasyk K.A.,
RA Speer M.C., Peters K.G., Marchuk D.A.;
RT "Allelic and locus heterogeneity in inherited venous malformations.";
RL Hum. Mol. Genet. 8:1279-1289(1999).
CC -!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE
CC RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
CC MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
CC ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
CC PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
CC FORMATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS
CC AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
CC ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
CC -!- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
CC MALFORMATIONS (VMCM1), AN ERROR OF VASCULAR MORPHOGENESIS
CC CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.

[illegible]

Seq	SEQUENCE	1124 AA:	125810 MW:	65BC05D18FA4CCEC	CRC64:
QY	Query Match	100.0%	Score 1708:	DB 1:	Length 1124:
Db	Best Local Similarity	100.0%	Pred. No. 8e-122:		
	Matches 323:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
QY	1 ALNRKVKNNPPPTIYPLVDMDNDIKQDYVIGSGNFQVYLKARKTKDGLRMDAIIKRKXEYA 60				
Db	802 ALNRKVKNNPPPTIYPLVDMDNDIKQDYVIGSGNFQVYLKARKTKDGLRMDAIIKRKXEYA 861				
QY	61 SKMDHRRDAGAELEVLCKIGHHPHNIINLGGACRHRYLYLAIEYADPHGNLDFLRKSRVIE 120				
Db	862 SKDHRDRDAGELEVLCKIGHHPHNIINLGGACRHRYLYLAIEYADPHGNLDFLRKSRVIE 921				
QY	121 TDPARAINSTASTLSSOOLHFAADVARGMYLSOKOPIHRDLAARNILVGENYAKIA 180				
Db	922 TDPARAINSTASTLSSOOLHFAADVARGMYLSOKOPIHRDLAARNILVGENYAKIA 981				
QY	181 DEGLSGQGVYKTKMGRLCPVRMMATIESLNTSVYTTNSDVAWSYGVLLMEIVSLGCTPYCG 240				
Db	982 DEGLSGQGVYKTKMGRLCPVRMMATIESLNTSVYTTNSDVAWSYGVLLMEIVSLGCTPYCG 1041				
QY	241 MTCAELEYEKLPGYRLKEPLNCDDEYEDLMROCWRKPYERPSPFAOILVSLNMLEBKRT 300				
Db	1042 MTCAELEYEKLPGYRLKEPLNCDDEYEDLMROCWRKPYERPSPFAOILVSLNMLEBKRT 1101				
QY	301 YVNTTLYEKETAYAGIDCSAEFAA 323				
Db	1102 YVNTTLYEKETAYAGIDCSAEFAA 1124				